

SEQUENCE LISTING

<110> FRANKARD, VALERIE
MIRONOV, VLADIMIR

<120> PLANTS HAVING MODIFIED GROWTH CHARACTERISTICS AND A METHOD FOR
MAKING THE SAME

<130> 4559-061539

<140> 10/580,085

<141> 2007-05-09

<150> PCT/EP2004/053030

<151> 2004-11-19

<150> 60/528,113

<151> 2003-12-09

<150> EP 03104280.7

<151> 2003-11-19

<160> 37

<170> PatentIn version 3.5

<210> 1

<211> 1428

<212> DNA

<213> Nicotiana tabacum

<220>

<223> Seedyl coding sequence (CDS0689)

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ctgaaacccc tttcggttag gccatcagat tcctttgaat ctgatttgtc aagtaaggaa	180
aatcaaactc ctttatttga gaattcatct gttaatctct catctccgtt acccataaag	240
ccacttaacc ctaatggggc tctggaaaat tcaagactca agccgaacaa gcccaattcc	300
aaacagagtc ttgatgagat ggcggctaga aagagcggaa agggaaatga tttccgtgat	360
gagaagaaaa tagacgagga aattgaagaa attcagatgg agattagtag gttgagttca	420
agattagagg ctttgagaat tgaaaaggct gagaaaactg ttgctaagac tgttgaaaag	480
cgaggaaggg ttgtggcagc aaagtttatg gagccaaaac aaagtgttat taagattgaa	540
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ccatctgaga tttttactgg aacgcggcgg cgaggggttg gtatggggcc atcagatatt	660
ctagcagggg caacaaaggc acggcaattg ggaaagcaag agatgattat tactcctatt	720

cagccaatac aaaacaggcg aaagtcgtgt ttttggaagc ttcaagagat tgaagaagag	780
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gataagaaac ggtcgttattc tgtagggaaa acgcgtgtgt ctcaaactga gagcaagaat	1140
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atgatagagt tgataggcaa gaaatcgttt ttcagtagtg atgaagataa ggagccacct	1380
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<210> 2

<211> 475

<212> PRT

<213> Nicotiana tabacum

<220>

<223> Seedyl protein (CDS0689)

<400> 2

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Ile	Trp	Asn	Asn	Ala	Ala	Phe	Asp	Asn	Gly	Asp	Ser	Glu	Asp	Leu	Ser
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Ser	Leu	Lys	Arg	Ser	Trp	Ser	Pro	Leu	Lys	Pro	Leu	Ser	Val	Arg	Pro
		35					40					45			

Ser	Asp	Ser	Phe	Glu	Ser	Asp	Leu	Ser	Ser	Lys	Glu	Asn	Gln	Thr	Pro
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Leu	Phe	Glu	Asn	Ser	Ser	Val	Asn	Leu	Ser	Ser	Pro	Leu	Pro	Ile	Lys
65					70					75					80

Pro	Leu	Asn	Pro	Asn	Gly	Ala	Leu	Glu	Asn	Ser	Arg	Leu	Lys	Pro	Asn
			85						90					95	

Lys Pro Asn Ser Lys Gln Ser Leu Asp Glu Met Ala Ala Arg Lys Ser
100 105 110

Gly Lys Gly Asn Asp Phe Arg Asp Glu Lys Lys Ile Asp Glu Glu Ile
115 120 125

Glu Glu Ile Gln Met Glu Ile Ser Arg Leu Ser Ser Arg Leu Glu Ala
130 135 140

Leu Arg Ile Glu Lys Ala Glu Lys Thr Val Ala Lys Thr Val Glu Lys
145 150 155 160

Arg Gly Arg Val Val Ala Ala Lys Phe Met Glu Pro Lys Gln Ser Val
165 170 175

Ile Lys Ile Glu Glu Arg Ile Ser Met Ser Ala Arg Thr Lys Val Glu
180 185 190

Gln Arg Arg Gly Leu Ser Leu Gly Pro Ser Glu Ile Phe Thr Gly Thr
195 200 205

Arg Arg Arg Gly Leu Ser Met Gly Pro Ser Asp Ile Leu Ala Gly Thr
210 215 220

Thr Lys Ala Arg Gln Leu Gly Lys Gln Glu Met Ile Ile Thr Pro Ile
225 230 235 240

Gln Pro Ile Gln Asn Arg Arg Lys Ser Cys Phe Trp Lys Leu Gln Glu
245 250 255

Ile Glu Glu Glu Gly Lys Ser Ser Ser Leu Ser Pro Lys Ser Arg Lys
260 265 270

Thr Ala Ala Arg Thr Met Val Thr Thr Arg Gln Ala Val Thr Thr Ile
275 280 285

Ala Ser Lys Lys Asn Leu Lys Lys Asp Asp Gly Leu Leu Ser Ser Val
290 295 300

Gln Pro Lys Lys Leu Phe Lys Asp Leu Glu Lys Ser Ala Ala Ala Asn
305 310 315 320

Lys Lys Pro Gln Arg Pro Gly Arg Val Val Ala Ser Arg Tyr Asn Gln
325 330 335

Ser Thr Ile Gln Ser Ser Val Val Arg Lys Arg Ser Leu Pro Glu Asn
340 345 350

Asp Lys Asp Glu Ser Lys Arg Asn Asp Lys Lys Arg Ser Leu Ser Val
355 360 365

Gly Lys Thr Arg Val Ser Gln Thr Glu Ser Lys Asn Leu Gly Thr Glu
370 375 380

Ser Arg Val Lys Lys Arg Trp Glu Ile Pro Ser Glu Ile Val Val His
385 390 395 400

Gly Asn Thr Glu Ser Glu Lys Ser Pro Leu Ser Ile Ile Val Lys Pro
405 410 415

Asp Leu Leu Pro Arg Ile Arg Ile Ala Arg Cys Val Asn Glu Thr Leu
420 425 430

Arg Asp Ser Gly Pro Ala Lys Arg Met Ile Glu Leu Ile Gly Lys Lys
435 440 445

Ser Phe Phe Ser Ser Asp Glu Asp Lys Glu Pro Pro Val Cys Gln Val
450 455 460

Leu Ser Phe Ala Glu Glu Asp Ala Glu Glu Glu
465 470 475

<210> 3
<211> 1336
<212> DNA
<213> Oryza sativa

<220>
<223> Seedy1 coding sequence

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ggcgacaagg agaatcaccg ccccgagggt gttgatgtcg ccgccggcta cgacgtcgag 180
gccgagatcg gccacatcga ggcggagatc ctgcgcctct cgtccccggct ccaccatctc 240
cgcgtctcca agcagccgga gccaaccgc gacgacgctc cgatggggga gatggtcgcg 300
aaggtgaggc cccggccgag gggcctcagc ctcgggcccc tggatgtgat ctccatcgtc 360

aatcgtgaga agcatccgct ggcacccaag cagcctccgg cgacgcgggg cagggggctc	420
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cagcaacagc aacgcgctgg cacggcgcg atcctgaagc caatcaagga gcctccggtg	540
cagcgtcgca ggggcgtcag cctcgggccg ttggagatcc accacggcgt cggcagcaag	600
gcaccagcgg cggcgcgagc caagccgttc accaccaagc tcaacgccat tcgagaagaa	660
acccgaccct ccaagcaatt cgccgtcccc gccaaagccat ggccgtcgag caatacaagg	720
cagacactgg actcgaggca aggaacagca gcaagtcgag cgaaggcgag gagcccgagc	780
cccaggcca ggaggcaatc caatggcaag gctactgaca caaggggagg caacaagggtg	840
gtggatgagc tcaagcccaa aggtgcgtcg tcaagtcaga gcggcagcgc cgccgccgcc	900
gccactgcca agaggatggc ggggagctcc aagatgaggg tcatcccgag ccgctacagc	960
ctcactcctg gcgcttccct tggaagcagt ggagcacagg agaggcgacg caagcagtct	1020
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ccttccaatg atccactctc tcctcaaacg atctccaagg ttgctgaaat gctcccaaag	1140
atcaggacca tgccgcctcc tgacgagagc cctcgcgatt ccggatgcgc caagcggggtt	1200
gccgaattgg tcgggaagcg ctcggttcttc acggctgcag ccgaggacgg gcgggcgctc	1260
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 <212> PRT
 <213> Oryza sativa

<220>
 <223> Seedy1 protein

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Ala Phe Asp Asp Ser Ser Cys Ser Arg Ser Ala Trp Leu Pro Gln Ser
 20 25 30

Pro Ala Val Ala Ala Val Arg Lys Gly Asp Lys Glu Asn His Arg Pro
 35 40 45

Glu Val Val Asp Val Ala Ala Gly Tyr Asp Val Glu Ala Glu Ile Gly

50

55

60

His Ile Glu Ala Glu Ile Leu Arg Leu Ser Ser Arg Leu His His Leu
65 70 75 80

Arg Val Ser Lys Gln Pro Glu Pro Asn Arg Asp Asp Ala Pro Met Gly
85 90 95

Glu Met Val Ala Lys Val Arg Pro Arg Pro Arg Gly Leu Ser Leu Gly
100 105 110

Pro Leu Asp Val Ile Ser Ile Val Asn Arg Glu Lys His Pro Leu Arg
115 120 125

Thr Lys Gln Pro Pro Ala Thr Arg Gly Arg Gly Leu Ser Leu Gly Pro
130 135 140

Met Glu Ile Ala Ala Ala Asn Pro Arg Val Pro Ala Ala Ala Gln His
145 150 155 160

Gln Gln Gln Gln Arg Ala Gly Thr Ala Arg Ile Leu Lys Pro Ile Lys
165 170 175

Glu Pro Pro Val Gln Arg Arg Arg Gly Val Ser Leu Gly Pro Leu Glu
180 185 190

Ile His His Gly Val Gly Ser Lys Ala Pro Ala Ala Ala Arg Ala Lys
195 200 205

Pro Phe Thr Thr Lys Leu Asn Ala Ile Arg Glu Glu Thr Arg Pro Ser
210 215 220

Lys Gln Phe Ala Val Pro Ala Lys Pro Trp Pro Ser Ser Asn Thr Arg
225 230 235 240

Gln Thr Leu Asp Ser Arg Gln Gly Thr Ala Ala Ser Arg Ala Lys Ala
245 250 255

Arg Ser Pro Ser Pro Arg Pro Arg Arg Gln Ser Asn Gly Lys Ala Thr
260 265 270

Asp Thr Arg Gly Gly Asn Lys Val Val Asp Glu Leu Lys Pro Lys Gly
275 280 285

Ala Ser Ser Ser Gln Ser Gly Ser Ala Ala Ala Ala Thr Ala Lys
290 295 300

Arg Met Ala Gly Ser Ser Lys Met Arg Val Ile Pro Ser Arg Tyr Ser
305 310 315 320

Leu Thr Pro Gly Ala Ser Leu Gly Ser Ser Gly Ala Gln Glu Arg Arg
325 330 335

Arg Lys Gln Ser Leu Pro Gly Ser Ser Gly Asp Ala Asn Gln Asn Glu
340 345 350

Glu Ile Arg Ala Lys Val Ile Glu Pro Ser Asn Asp Pro Leu Ser Pro
355 360 365

Gln Thr Ile Ser Lys Val Ala Glu Met Leu Pro Lys Ile Arg Thr Met
370 375 380

Pro Pro Pro Asp Glu Ser Pro Arg Asp Ser Gly Cys Ala Lys Arg Val
385 390 395 400

Ala Glu Leu Val Gly Lys Arg Ser Phe Phe Thr Ala Ala Ala Glu Asp
405 410 415

Gly Arg Ala Leu Asp Val Glu Ala Pro Glu Ala Val Ala Glu Ala
420 425 430

<210> 5
<211> 1860
<212> DNA
<213> Medicago trunculata

<220>
<223> Seedyl coding sequence

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aatcacatcg gagcgtgtat gagtagccgt ttcacatcca acggccagta agagcgtaac 180
tttattttctt ccctcttcaa tctccaacgg tcacataatc tcttccaaat acaaataatt 240
ccctctttca acctcactct tcattttcttc aacccaaacc caaaaaacta atcagattct 300
tcttaaattct tgaaaccttt ctcccaaaaag cacttaaata aaaaagcact taaccatgaa 360
taacacaaac aacaacaaca ttctttcttca ttccacacag gttcaagtgt ggaacaacgc 420

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tgcggaatt gaaagtgaaa ttaagcgatt aacttcgaag ctggaattgc ttcgtgttga	600
aaaagctgaa agaaaaatcg cttctgaaaa gcgtgttagt ggaattggta ctggaagaat	660
agtagcagcg aagtttatgg aaccgaagaa aaacgttaca ccgaaacgaa acggtgtcgt	720
tttcaaggag gagacaccga aacgaaacgg tgtcgtttcg gatacgccga aatctagggt	780
taattggaga agagggatga gttaggtcc gatggagatt gccgggaaaag tgatggcacc	840
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accgaatttg aatttgaatt caaattcagt taattctgcg gttggatcga ttaagcgtgt	1080
gaagaagaaa gatgaagaaa ttgctcaggt tcaaccgaag aagctgtttg aaggtgaaaa	1140
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aatcagggct aagaagagat gggagatacc aattgaagaa gtggatgtga gtggttttgt	1320
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tgaaataata acaacaagca tgtgtcttgc ttaataattg tatattgttt tgtttgtttt	1740
ataatgatat ggatttaatt tgtatacaca atataatata gtatgcattg agagagtttt	1800
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<211> 394

<212> PRT

<213> Medicago trunculata

<220>

<223> Seedy1 protein

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Ser Ser Ser Asp Ser Ile Lys Glu Asn Leu Asn Pro Ser Ala Phe Asn
35 40 45

Ile Val Pro Ser Ser Asn Lys Arg Thr Ile Asp Asp Glu Ile Ala Glu
50 55 60

Ile Glu Ser Glu Ile Lys Arg Leu Thr Ser Lys Leu Glu Leu Leu Arg
65 70 75 80

Val Glu Lys Ala Glu Arg Lys Ile Ala Ser Glu Lys Arg Val Ser Gly
85 90 95

Ile Gly Thr Gly Arg Ile Val Ala Ala Lys Phe Met Glu Pro Lys Lys
100 105 110

Asn Val Thr Pro Lys Arg Asn Gly Val Val Phe Lys Glu Glu Thr Pro
115 120 125

Lys Arg Asn Gly Val Val Ser Asp Thr Pro Lys Ser Arg Val Asn Trp
130 135 140

Arg Arg Gly Met Ser Leu Gly Pro Met Glu Ile Ala Gly Lys Val Met
145 150 155 160

Ala Pro Pro Ala Met Thr Ile Thr Pro Ala Thr Val Asn Arg Arg Lys
165 170 175

Ser Cys Phe Trp Lys Pro Gln Glu Ser Cys Glu Val Met Pro Ser Gly
180 185 190

Ile Thr Pro Ala Thr Val Asn Arg Arg Lys Ser Cys Phe Leu Lys Pro
195 200 205

Gln Glu Ser Cys Glu Glu Asn Arg Arg Lys Thr Ile Cys Lys Pro Asn
210 215 220

Leu Asn Leu Asn Ser Asn Ser Val Asn Ser Ala Val Gly Ser Ile Lys
225 230 235 240

Arg Val Lys Lys Lys Asp Glu Glu Ile Ala Gln Val Gln Pro Lys Lys
245 250 255

Leu Phe Glu Gly Glu Lys Ser Val Lys Lys Ser Leu Lys Gln Gly Arg
260 265 270

Ile Val Ala Ser Arg Tyr Asn Ser Gly Gly Gly Gly Gly Asp Ala Arg
275 280 285

Lys Arg Ser Phe Ser Glu Asn Asn Lys Gly Leu Gly Ser Glu Ile Arg
290 295 300

Ala Lys Lys Arg Trp Glu Ile Pro Ile Glu Glu Val Asp Val Ser Gly
305 310 315 320

Phe Val Met Leu Pro Lys Ile Ser Thr Met Arg Phe Val Asp Glu Ser
325 330 335

Pro Arg Asp Ser Gly Ala Val Lys Arg Val Ala Glu Leu Asn Gly Lys
340 345 350

Arg Ser Tyr Phe Cys Asp Glu Asp Glu Glu Glu Arg Val Met Val Glu
355 360 365

Glu Glu Gly Gly Ser Val Cys Gln Val Leu Asn Phe Ala Glu Asp Asp
370 375 380

Asp Asp Asp Asp Asp Tyr Gly Glu Gln Gly
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<210> 7
<211> 674
<212> DNA
<213> Saccharum sp.

<220>
<223> Seedyl coding sequence (partial 5' end)

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<221> modified_base
<222> (362)..(362)
<223> a, c, t or g

<220>
<221> modified_base
<222> (372)..(372)

<223> a, c, t or g

<220>

<221> modified_base

<222> (674)..(674)

<223> a, c, t or g

<400> 7

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tccggtccag ggggctctcc ggcggcggtg gcgatggagg aggaccgct catcccgtg      180
gtgcacgtct ggaacaacgc cgccttcgac cagcctcct cctccgctg gcacgccac      240
tcccctgtgc ccgcgagcgc acgtcgcgag gcggaggggg acaaggagaa ccaccgcccc      300
gaccccgacc ccgacgtcga ggcggagatc ggccacatcg aggcgagat cctgcgcctg      360
tntcccgcc tncaccacct tcgcacctcc aagcagtcgg agccgtccaa gcgcggagag      420
gtcgcgcccc cgcccgcggc gaaggcgaaa gcggcgggcg cggcgcggct gcggacgcgg      480
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gacaaccagc agcagcagcc gcgtgccgcg cagggctctga agccgatcaa gcaggccacg      600
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<210> 8

<211> 166

<212> PRT

<213> Saccharum sp.

<220>

<223> Seedyl protein (partial N term)

<220>

<221> MOD_RES

<222> (70)..(70)

<223> Any amino acid

<400> 8

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Ala Phe Asp His Ala Ser Ser Ser Ala Trp His Ala His Ser Pro Val
20           25          30
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Pro Ala Ser Ala Arg Arg Glu Ala Glu Gly Asp Lys Glu Asn His Arg
35           40          45
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Pro Asp Pro Asp Pro Asp Val Glu Ala Glu Ile Gly His Ile Glu Ala
50 55 60

Glu Ile Leu Arg Leu Xaa Ser Arg Leu His His Leu Arg Thr Ser Lys
65 70 75 80

Gln Ser Glu Pro Ser Lys Arg Gly Glu Val Ala Pro Ala Pro Ala Ala
85 90 95

Lys Ala Lys Ala Ala Ala Ala Ala Arg Leu Arg Thr Arg Gly Leu Ser
100 105 110

Leu Gly Pro Leu Asp Val Ala Ala Ala Gly Asn Pro Asn Pro Leu Thr
115 120 125

Thr Asp Asn Gln Gln Gln Gln Pro Arg Ala Ala Gln Gly Leu Lys Pro
130 135 140

Ile Lys Gln Ala Thr Ala Ala Ala Gly Lys Gly Val Arg Leu Gly Pro
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Leu Arg His Gly Arg Arg
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<210> 9
<211> 876
<212> DNA
<213> Zea mays

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<222> (869)..(869)
<223> a, c, t or g

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ggagcgaagc ggtcaatcac accagcaatg tagccacgac gaagaggccg gcggggagct 300
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<210> 10
 <211> 224
 <212> PRT
 <213> Zea mays

<220>
 <223> Seedy1 protein (partial C term)

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Ala Val Pro Ala Arg Pro Trp Pro Ser Ser Asn Ala Arg His Pro Leu
 20 25 30

Asp Ala Arg Gln Gly Thr Ala Ala Ser Arg Ala Lys Ala Arg Ser Gly
 35 40 45

Ser Ile Ser Pro Ser Arg Phe Arg Arg Gln Ser Thr Ser Lys Ala Ala
 50 55 60

Glu Thr Arg Ala Gly Asn Ala Lys Pro Thr Glu Ala Thr Arg Gly Gly
 65 70 75 80

Ser Glu Ala Val Asn His Thr Ser Asn Val Ala Thr Thr Lys Arg Pro
 85 90 95

Ala Gly Ser Ser Lys Val Arg Val Val Pro Ser Arg Tyr Ser Ile Pro
 100 105 110

Pro Gly Ser Ser Leu Ala Ala Val Thr Gln Gly Asn Arg Cys Lys Gln

115

120

125

Ser Leu Pro Gly Ser Ala Thr Glu Thr Arg Val Asn Leu Thr Glu Pro
 130 135 140

Pro Asn Asp Glu Leu Ser Pro Glu Glu Leu Ala Lys Val Ala Glu Leu
 145 150 155 160

Leu Pro Arg Ile Arg Thr Met Pro Pro Ser Asp Glu Ser Pro Arg Asp
 165 170 175

Ser Gly Cys Ala Lys Arg Val Ala Asp Leu Val Gly Lys Arg Ser Phe
 180 185 190

Phe Thr Ala Ala Gly Asp Asp Gly Asn Leu Val Thr Pro Tyr Gln Ala
 195 200 205

Arg Val Val Glu Leu Glu Ser Pro Glu Ala Ala Ala Glu Glu Ala Glu
 210 215 220

<210> 11

<211> 1257

<212> DNA

<213> Arabidopsis thaliana

<220>

<223> Seedyl coding sequence

<400> 11

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tctcacctca acgaatcatt cgattccgat tgtagcaagg agaatcagtt tccgatttcg 180

gtttcctctt cgctccaatc ctcagtctcg atcaccgaag ctccgtcagc aaaatccaag 240

accgtgaaga ccaaattccgc cgcagatcgg agtaaaaagc gagatatcga tgcagagatc 300

gaagaagtag agaaggagat cggacgatta tcgacgaaat tggagtcgct ccgattagag 360

aaggcggagc aaaccgcaag aagcattgct atacgtggaa gaatcggtcc ggccaagtgc 420

atggaatcat ctcagaaaca agtgaaattc gacgattcgt gttttacagg atcgaaatca 480

agagccactc gtagaggcgt tagtcttgga ccagcggaga tattcaattc cgcgaagaaa 540

tctgaaaactg tgactcctct tcaatcagct cagaatcgac gcaagtcttg tttctttaag 600

cttcctggaa tcgaagaagg tcaagtgcgc acacgaggta aaggaagaac gagtttgagt 660

ctgagtccga gatctcgcaa agcgaaaatg acggcagctc agaagcaagc agctacgacg	720
gtggggtcaa agagagctgt gaagaaagaa gaaggagttc tcttaacaat ccagcctaag	780
aggctattca aagaagatga aaagaatggt tctttaagga aaccattgaa accaggaaga	840
gttggtggcta gtaggtacag tcaaattgggt aaaacgcaga ctggagagaa agatgttagg	900
aaaaggctcgt tgcctgagga tgaagagaaa gagaatcata agaggtcgga gaagagaaga	960
gcttctgatg aaagtaacaa gagtgaaggg agagtgaaga agagatggga gattccaagt	1020
gaagttgatc tgtatagcag tggtgagaac ggtgacgagt ctcctatagt taaggagcta	1080
cctaagatca gaacgcttcg tcgtgtggga gggagccctc gtgattcagg tgctgctaag	1140
agagttgcag aattacaagc caaggatcgt aacttcactt tttgccagct tctgaagttt	1200
gaagaatgaa tgatccgctt atcaatttga gtaaaatcca caactcttgt tgtgggtt	1257

<210> 12
 <211> 402
 <212> PRT
 <213> Arabidopsis thaliana

<220>
 <223> Seedy1 protein

<400> 12

Met	Thr	Ser	Ile	Glu	Ala	Thr	Glu	Thr	Leu	Asn	Ala	Pro	Pro	Lys	Leu
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Gln	Ile	Trp	Asn	Asn	Ala	Ala	Phe	Asp	Asp	Gly	Asp	Ser	Gln	Ile	Thr
			20					25					30		
Ser	Ala	Ile	Glu	Ala	Ser	Ser	Trp	Ser	His	Leu	Asn	Glu	Ser	Phe	Asp
			35				40					45			
Ser	Asp	Cys	Ser	Lys	Glu	Asn	Gln	Phe	Pro	Ile	Ser	Val	Ser	Ser	Ser
	50					55					60				
Leu	Gln	Ser	Ser	Val	Ser	Ile	Thr	Glu	Ala	Pro	Ser	Ala	Lys	Ser	Lys
65					70				75					80	
Thr	Val	Lys	Thr	Lys	Ser	Ala	Ala	Asp	Arg	Ser	Lys	Lys	Arg	Asp	Ile
			85					90					95		
Asp	Ala	Glu	Ile	Glu	Glu	Val	Glu	Lys	Glu	Ile	Gly	Arg	Leu	Ser	Thr
			100					105					110		

Lys Leu Glu Ser Leu Arg Leu Glu Lys Ala Glu Gln Thr Ala Arg Ser
 115 120 125

Ile Ala Ile Arg Gly Arg Ile Val Pro Ala Lys Phe Met Glu Ser Ser
 130 135 140

Gln Lys Gln Val Lys Phe Asp Asp Ser Cys Phe Thr Gly Ser Lys Ser
 145 150 155 160

Arg Ala Thr Arg Arg Gly Val Ser Leu Gly Pro Ala Glu Ile Phe Asn
 165 170 175

Ser Ala Lys Lys Ser Glu Thr Val Thr Pro Leu Gln Ser Ala Gln Asn
 180 185 190

Arg Arg Lys Ser Cys Phe Phe Lys Leu Pro Gly Ile Glu Glu Gly Gln
 195 200 205

Val Thr Thr Arg Gly Lys Gly Arg Thr Ser Leu Ser Leu Ser Pro Arg
 210 215 220

Ser Arg Lys Ala Lys Met Thr Ala Ala Gln Lys Gln Ala Ala Thr Thr
 225 230 235 240

Val Gly Ser Lys Arg Ala Val Lys Lys Glu Glu Gly Val Leu Leu Thr
 245 250 255

Ile Gln Pro Lys Arg Leu Phe Lys Glu Asp Glu Lys Asn Val Ser Leu
 260 265 270

Arg Lys Pro Leu Lys Pro Gly Arg Val Val Ala Ser Arg Tyr Ser Gln
 275 280 285

Met Gly Lys Thr Gln Thr Gly Glu Lys Asp Val Arg Lys Arg Ser Leu
 290 295 300

Pro Glu Asp Glu Glu Lys Glu Asn His Lys Arg Ser Glu Lys Arg Arg
 305 310 315 320

Ala Ser Asp Glu Ser Asn Lys Ser Glu Gly Arg Val Lys Lys Arg Trp
 325 330 335

Glu Ile Pro Ser Glu Val Asp Leu Tyr Ser Ser Gly Glu Asn Gly Asp
 340 345 350

Glu Ser Pro Ile Val Lys Glu Leu Pro Lys Ile Arg Thr Leu Arg Arg
 355 360 365

Val Gly Gly Ser Pro Arg Asp Ser Gly Ala Ala Lys Arg Val Ala Glu
 370 375 380

Leu Gln Ala Lys Asp Arg Asn Phe Thr Phe Cys Gln Leu Leu Lys Phe
 385 390 395 400

Glu Glu

<210> 13

<211> 3074

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
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 polynucleotide

<400> 13

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ttattgtaaa gttctacaaa gctaatttaa aagttattgc attaacttat ttcataattac	180
aaacaagagt gtcaatggaa caatgaaaac catatgacat actataattt tgttttttatt	240
attgaaatta tataattcaa agagaataaa tccacatagc cgtaaagttc tacatgtggt	300
gcattaccaa aatatatata gcttacaaaa catgacaagc ttagtttgaa aaattgcaat	360
ccttatcaca ttgacacata aagtgagtga tgagtcataa tattattttc ttgctaccc	420
atcatgtata tatgatagcc acaaagttac tttgatgatg atatcaaaga acatttttag	480
gtgcacctaa cagaatatcc aaataatatg actcacttag atcataatag agcatcaagt	540
aaaactaaca ctctaaagca accgatggga aagcatctat aaatagacaa gcacaatgaa	600
aatcctcatc atccttcacc acaattcaaa tattatagtt gaagcatagt agtaatttaa	660
atcaactagg gatatcaciaa gtttgtacaa aaaagcaggc tggtagcggg cgggaattcc	720
cgggatatcg tcgaccacg cgtccgctga cgcgtggggt ccactacatc aagacatcta	780
ctacactcat cttttttgca cttattgggt gtaaattttt gaaacccagt tgagaaaaat	840
gagtgtgtta caatacccag aagggattga cccagcagat gttcagatat ggaacaatgc	900
agcatttgat aatggagatt ctgaagattt gtcttcgctg aaacgttcctt ggtctcctct	960

gaaaccccctt tccggttaggc catcagattc ctttgaatct gatttgtcaa gtaaggaaaa	1020
tcaaactcct ttatttgaga attcatctgt taatctctca tctccgttac ccataaagcc	1080
acttaaccct aatggggctc tggaaaattc aagactcaag ccgaacaagc ccaattccaa	1140
acagagtctt gatgagatgg cggctagaaa gagcggaaaag ggaaatgatt tccgtgatga	1200
gaagaaaata gacgaggaaa ttgaagaaat tcagatggag attagtaggt tgagttcaag	1260
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aggaagggtt gtggcagcaa agtttatgga gccaaaacaa agtgttatta agattgaaga	1380
gcgtatatca atgagtgcaa gaacaaaggt ggagcagaga aggggtctta gtttaggacc	1440
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gccaatacaa aacaggcgaa agtcgtgttt ttggaagctt caagagattg aagaagaggg	1620
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aaggcaggca gttactacaa ttgcatcaaa gaagaatttg aaaaaagatg atggactttt	1740
gagttcagtt cagccaaaga agttgtttaa agatctcgaa aagtctgctg ctgctaataa	1800
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taagaaacgg tcgttatctg tagggaaaac gcgtgtgtct caaactgaga gcaagaatth	1980
gggtactgaa agtaggggtga aaaagagatg ggaaattcct agtgagattg tagttcatgg	2040
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gatgattgag taataatgtg tcacgcatca ccatgggtgg cagtgtcagt gtgagcaatg	2700

acctgaatga acaattgaaa tgaaaagaaa aaaagtactc catctgttcc aaattaaaaat	2760
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atttgttatc atccgggagg tcttctaggg ataacagggt aattatatcc ctctagacaa	2880
cacacaacaa ataagagaaa aaacaaataa tattaatttg agaatgaaca aaaggaccat	2940
atcattcatt aactcttctc catccatttc catttcacag ttcgatagcg aaaaccgaat	3000
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cataatactc gaac	3074

<210> 14
 <211> 668
 <212> DNA
 <213> Oryza sativa

<220>
 <223> Prolamin RP6 promoter sequence

<400> 14	
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gttattgtaa agttctacaa agctaattta aaagttattg cattaactta tttcatatta	180
caaacaagag tgtcaatgga acaatgaaaa ccatatgaca tactataatt ttgtttttat	240
tattgaaatt atataattca aagagaataa atccacatag ccgtaaagtt ctacatgtgg	300
tgcattacca aaatatatat agcttacaaa acatgacaag cttagtttga aaaattgcaa	360
tccttatcac attgacacat aaagtgagt atgagtcata atattatttt tcttgctacc	420
catcatgtat atatgatagc cacaaagtta ctttgatgat gatatcaaag aacattttta	480
ggtgcaccta acagaatatc caaataatat gactcactta gatcataata gagcatcaag	540
taaaactaac actctaaagc aaccgatggg aaagcatcta taaatagaca agcacaatga	600
aaatcctcat catccttcac cacaattcaa atattatagt tgaagcatag tagtagaatc	660
caacaaca	668

<210> 15
 <211> 12
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (1)..(2)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (3)..(3)
<223> Val, Leu or His

<220>
<221> MOD_RES
<222> (4)..(4)
<223> Gln or His

<220>
<221> MOD_RES
<222> (5)..(5)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (7)..(7)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (10)..(10)
<223> Ala or Pro

<220>
<221> MOD_RES
<222> (11)..(11)
<223> Phe or Cys

<220>
<223> See specification as filed for detailed description of
substitutions and preferred embodiments

<400> 15
Xaa Xaa Xaa Xaa Xaa Trp Xaa Asn Ala Xaa Xaa Asp
1 5 10

<210> 16
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Motif 2 CORE peptide

<220>
<221> MOD_RES
<222> (4)..(5)
<223> Any amino acid

<400> 16
Lys Glu Asn Xaa Xaa Pro
1 5

<210> 17
<211> 26
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Ile, Val or Ala

<220>
<221> MOD_RES
<222> (2)..(2)
<223> Asp or Glu

<220>
<221> MOD_RES
<222> (3)..(3)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (5)..(5)
<223> Ile or Met

<220>
<221> MOD_RES
<222> (6)..(7)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (8)..(8)
<223> Ile or Val

<220>
<221> MOD_RES
<222> (9)..(9)
<223> Glu or Gln

<220>
<221> MOD_RES
<222> (10)..(10)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (12)..(13)

<223> Any amino acid

<220>

<221> MOD_RES

<222> (16)..(16)

<223> Any amino acid

<220>

<221> MOD_RES

<222> (17)..(17)

<223> Ser, Thr, Leu, Ile or Ala

<220>

<221> MOD_RES

<222> (18)..(18)

<223> Arg or Lys

<220>

<221> MOD_RES

<222> (20)..(21)

<223> Any amino acid

<220>

<221> MOD_RES

<222> (24)..(24)

<223> Leu, Val, Thr or Ile

<220>

<221> MOD_RES

<222> (25)..(25)

<223> Any amino acid

<220>

<221> MOD_RES

<222> (26)..(26)

<223> Lys or Gln

<220>

<223> See specification as filed for detailed description of
substitutions and preferred embodiments

<400> 17

Xaa	Xaa	Xaa	Glu	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Glu	Xaa	Xaa	Arg	Leu	Xaa
1				5				10						15	

Xaa	Xaa	Leu	Xaa	Xaa	Leu	Arg	Xaa	Xaa	Xaa
			20				25		

<210> 18

<211> 29

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<220>
<221> MOD_RES
<222> (3)..(3)
<223> Arg or Lys

<220>
<221> MOD_RES
<222> (5)..(5)
<223> Arg, Ser or Lys

<220>
<221> MOD_RES
<222> (6)..(6)
<223> Thr or Ile

<220>
<221> MOD_RES
<222> (7)..(7)
<223> Met, Leu, Ala or Val

<220>
<221> MOD_RES
<222> (8)..(8)
<223> Pro or Arg

<220>
<221> MOD_RES
<222> (9)..(10)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (11)..(11)
<223> Asp, Gln, Thr or Asn

<220>
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<222> (12)..(12)
<223> Glu or Gly

<220>
<221> MOD_RES
<222> (13)..(13)
<223> Ser or Thr

<220>
<221> MOD_RES
<222> (14)..(14)
<223> Pro or Leu

<220>
<221> MOD_RES
<222> (19)..(19)
<223> Cys, Pro or Ala

<220>
<221> MOD_RES
<222> (20)..(20)

<223> Ala, Val or Ile

<220>

<221> MOD_RES

<222> (23)..(23)

<223> Val, Gln, Asn or Ile

<220>

<221> MOD_RES

<222> (24)..(24)

<223> Ala or Ile

<220>

<221> MOD_RES

<222> (25)..(25)

<223> Asp or Glu

<220>

<221> MOD_RES

<222> (26)..(26)

<223> Leu or Arg

<220>

<221> MOD_RES

<222> (27)..(27)

<223> Val, Gln, Asn or Ile

<220>

<221> MOD_RES

<222> (28)..(28)

<223> Gly or Ala

<220>

<223> See specification as filed for detailed description of
substitutions and preferred embodiments

<400> 18

Leu	Pro	Xaa	Ile	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Arg	Asp
1			5				10							15	

Ser	Gly	Xaa	Xaa	Lys	Arg	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Lys
		20				25						

<210> 19

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
6xHis tag

<400> 19

His	His	His	His	His	His
1			5		

<210> 20
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 20
tttttttttt tttttttttt ttttt

25

<210> 21
<211> 81
<212> PRT
<213> Arabidopsis thaliana

<400> 21
Met Met Glu Glu Asp Pro Leu Ile Pro Leu Val His Val Trp Thr Asn
1 5 10 15

Ala Ala Phe Asp Ser Ser Ser Ser Ser Ser Ala Trp His Ala His Ala
20 25 30

Thr Pro Val Arg Arg Gly Glu Lys Glu Asn Arg Arg Pro Ala Glu Thr
35 40 45

Asn Asp Ala Asp Ala Glu Ile Ala Arg Ile Glu Ala Glu Ile Leu Arg
50 55 60

Leu Ser Ser Arg Leu His His Leu Arg Val Ser Lys Gly His Asp Ala
65 70 75 80

Lys

<210> 22
<211> 84
<212> PRT
<213> Zea mays

<400> 22
Met Glu Glu Asp Pro Leu Ile Gln Leu Val His Val Trp Ser Asn Ala
1 5 10 15

Ala Cys Asp Asn Ala Ala Ala Ser Ser Ser Val Cys His Ala His Ser
20 25 30

Pro Ala Pro Ala Ser Ala Arg Glu Gly Glu Gly Asp Lys Glu Asn Leu
35 40 45

Arg Arg Glu Pro Asp Val Glu Glu Glu Met Arg His Ile Glu Ala Glu
50 55 60

Ile Leu Arg Leu Ser Leu Arg Leu His His Leu Arg Thr Ser Gln Gln
65 70 75 80

Leu Gln Pro Pro

<210> 23
<211> 85
<212> PRT
<213> Saccharum sp.

<400> 23
Met Glu Glu Asp Pro Leu Ile Pro Leu Val His Val Trp Asn Asn Ala
1 5 10 15

Pro Phe Asp His Ala Ser Tyr Ser Ala Trp His Ala His Ser Pro Ala
20 25 30

Arg Ala Ser Ala Gly His Glu Ala Glu Gly Asp Lys Glu Asn His Arg
35 40 45

Pro Asp Pro Asp Pro Asp Val Glu Ala Glu Ile Gly His Ile Glu Ala
50 55 60

Glu Ile Leu Arg Leu Ser Ser Arg Leu His His Leu Arg Thr Ser Lys
65 70 75 80

Gln Ser Glu Pro Pro
85

<210> 24
<211> 125
<212> PRT
<213> Brassica napus

<400> 24
Met Thr Ser Thr Glu His Thr Glu Thr Leu Asn Ala Pro Glu Leu Gln
1 5 10 15

Ile Trp Asn Asn Ala Ala Phe Asp Asp Gly Asp Ser Asn Leu Thr Ser
20 25 30

Ala Ile Glu Ala Ser Trp Ser Asn Leu Asn Ala Ser Phe Asp Ser Asp

35

40

45

Cys Ser Lys Glu Asn Gln Ile Pro Val Ser Val Ser Ser Ser Leu Lys
 50 55 60

Ser Ser Val Ser Phe Ser Thr Asp Asp Pro Ile Arg Cys Gly Lys Val
 65 70 75 80

Lys Glu Lys Pro His Lys Thr Gly Lys Val Arg His Gly Asp Ile Asp
 85 90 95

Ala Glu Ile Glu Glu Val Glu Lys Glu Met Asn Arg Leu Ser Ile Arg
 100 105 110

Leu Glu Ser Leu Arg Leu Glu Lys Ala Glu Gln Ile Ala
 115 120 125

<210> 25

<211> 86

<212> PRT

<213> *Eschscholzia californica*

<400> 25

Met Leu Glu Ile Ser Glu Thr Leu Asn Leu Pro Asp Leu Gln Thr Trp
 1 5 10 15

Asn Asn Ala Ala Phe Asp Ser Gly Ser Thr Asp Asn His Thr Thr Ala
 20 25 30

Ile Lys Ala Ser Ser Ser Pro Leu Lys Pro Ile Val Leu Asn Gln Ser
 35 40 45

Glu Pro Ser Ile Leu Asp Ser Ile Tyr Thr Lys Glu Asn Gln Thr Pro
 50 55 60

Ser Cys Cys Ile Ser Pro Val Arg Thr Lys Ser Pro Leu Pro Ile Lys
 65 70 75 80

Pro Leu His Pro Asn Gly
 85

<210> 26

<211> 144

<212> PRT

<213> *Gossypium arboreum*

<400> 26

Met Ser Ile Leu Gln Tyr Pro Asp Ser Phe Asn Val Pro Glu Leu Gln
 1 5 10 15
 Val Trp Asn Asn Ala Ala Phe Asp Asn Gly Asp Ser Glu Asp Thr Asn
 20 25 30
 Ala Ile Lys Asp Ser Trp Cys Asn Phe Asn Ser Gly Ser Val Asn Gln
 35 40 45
 Ser Leu Glu Ser Asp Gly Ser Lys Glu Asn Gln Ser Pro Leu Trp Ile
 50 55 60
 Lys Ser Pro Val Ser Phe Lys Ser Thr Ala Ser Val Val Lys Pro Leu
 65 70 75 80
 Ser Ser Lys Asn Val Thr Gly Asn Thr Arg Glu Pro Phe Ser Ala Lys
 85 90 95
 Met Lys Ser Gly Val Cys Lys Glu Glu Glu Lys Lys Arg Asp Glu Lys
 100 105 110
 Lys Ile Asp Met Glu Ile Glu Glu Ile Glu Lys Glu Val Ala Arg Leu
 115 120 125
 Ser Ala Lys Leu Glu Ser Leu Arg Leu Glu Lys Pro Asn Ile Met Gln
 130 135 140
 <210> 27
 <211> 75
 <212> PRT
 <213> Populus tremula
 <400> 27
 Met Ser Ser Ile Leu Gln Tyr Pro Asp Val Val Asp Ala Pro Glu Val
 1 5 10 15
 Gln Ile Trp Asn Asn Ala Ala Phe Asp Asn Gly Glu Ser Glu Gly Ser
 20 25 30
 Leu Asn Leu Lys Ser Ser Trp Trp Asn Gln Ser Leu Glu Ser Asp Ala
 35 40 45
 Ser Lys Glu Asn Leu Ser Pro Val Cys Glu Gln Ser Ser Pro Val Phe
 50 55 60
 Val Asn Ser Ser Lys Pro Ala Lys Pro Leu Gln

65

70

75

<210> 28

<211> 77

<212> PRT

<213> *Plumbao zeylanica*

<400> 28

Met Asn Glu Val Leu His Leu Gln Glu Ala Ala Arg Thr Asp Ser Ser
 1 5 10 15

Thr Asp His Gln Ile Trp Asn Asn Ala Ala Phe Asp Ser Gly Glu Ser
 20 25 30

Glu Asp Ser Pro Val Val Ile Asp Phe Ser Ala Pro Asn Leu Ser Gln
 35 40 45

Ser Leu Leu Ser Asp Ser Ser Ile Lys Glu Asn Leu Ser Pro Ser Leu
 50 55 60

Ala Glu Met Pro His Pro Ala Lys Ser Pro Met Gln Lys
 65 70 75

<210> 29

<211> 139

<212> PRT

<213> *Citrus sinensis*

<400> 29

Met Ser Val Leu Gln Tyr Pro Asp Thr Leu Asn Gly Gln Glu Leu Gln
 1 5 10 15

Ile Trp Asn Asn Ala Ala Phe Asp Asn Gly Glu Ser Glu Asp Ser Thr
 20 25 30

Ala Met Lys Gly Ser Trp Ala Asn Leu Lys Ser Val Tyr Met Asn Gln
 35 40 45

Ser Leu Glu Ser Asp Cys Ser Lys Glu Asn Leu Ser Pro Arg Leu Asn
 50 55 60

Lys Ser Pro Thr Ser Ser Leu Lys Ser Cys Val Pro Asn Lys Pro Leu
 65 70 75 80

Gln Val Asn Ser Ser Val Lys Asn Ser Gln Met Lys Gln Leu Lys Ser
 85 90 95

Val Ser Lys Glu Glu Glu Thr Arg Asp Glu Arg Lys Ile Asp Ile Glu
 100 105 110

Ile Glu Glu Ile Glu Lys Glu Ile Ser Arg Leu Ser Ser Arg Leu Glu
 115 120 125

Ala Leu Arg Leu Glu Lys Ile Asp Ile Lys Thr
 130 135

<210> 30
 <211> 186
 <212> PRT
 <213> Hordeum vulgare

<400> 30
 Ile Ser Thr Ala Ser Thr Cys Arg Arg Pro Ala Gly Ser Ser Lys Val
 1 5 10 15

Arg Val Val Pro Ser Arg Tyr Ser Leu Met Pro Gly Ala Ser Leu Gly
 20 25 30

Ala Ala Thr Gln Asp Gly Arg Arg Lys Glu Ser Leu Pro Gly Ser Thr
 35 40 45

Gly Ser Thr Gly Gln Lys Glu Glu Ile Lys Ala Val Pro Thr Glu Pro
 50 55 60

Val Asp Asp Asp Leu Ser Pro Glu Ser Leu Asp Lys Val Ala Glu Leu
 65 70 75 80

Leu Pro Arg Ile Arg Thr Met Pro Arg Pro Asn Glu Thr Pro Pro Asp
 85 90 95

Ser Gly Cys Ala Lys Arg Ala Ala Asp Leu Val Gly Lys Arg Ser Phe
 100 105 110

Phe Ala Ala Ala Ala Ala Gly Asp Gly Ser Ala Ile Ser Ser Tyr Gln
 115 120 125

Ala Arg Val Leu Glu Ala Glu Ala Pro Glu Glu Ala Ala Ala Ala Gly
 130 135 140

Ala Leu Ser Asp Glu Ala Ala Ala Ala Gly Ala Leu Ser Asp Glu Ala
 145 150 155 160

Ala Ala Ala Ala Ala Ala Ala Glu Ala Leu Ser Asp Glu Ala Ala Ala

165

170

175

Ala Glu Ala Leu Ser Asp Glu Ala Ala Ala
 180 185

<210> 31

<211> 145

<212> PRT

<213> Triticum aestivum

<400> 31

Gly Arg Tyr Ser Leu Met Pro Gly Ala Ser Leu Gly Ala Ala Ser Gln
 1 5 10 15

Glu Arg Arg Arg Lys Glu Ser Leu Pro Gly Ser Thr Gly Gly Ala Gly
 20 25 30

Gln Lys Glu Glu Glu Ile Lys Ala Met Pro Thr Glu Pro Val Asp Asp
 35 40 45

Asp Leu Ser Pro Glu Ser Leu Asp Lys Val Ala Glu Leu Leu Pro Arg
 50 55 60

Thr Arg Thr Met Pro Pro Pro Asp Glu Thr Pro Arg Asp Ser Gly Cys
 65 70 75 80

Ala Lys Arg Ala Ala Asp Leu Val Gly Lys Arg Ser Phe Phe Ala Ala
 85 90 95

Ala Ala Ala Gly Asp Cys Ser Ala Ile Ser Ser Tyr Gln Ala Arg Val
 100 105 110

Leu Glu Ala Glu Ala Pro Glu Glu Ala Ala Ala Ala Glu Ala Leu
 115 120 125

Gly Asp Glu Ala Ala Ser Ala Gly Glu Ala Leu Gly Asp Glu Ala Ala
 130 135 140

Ala
 145

<210> 32

<211> 139

<212> PRT

<213> Zea mays

<400> 32

Thr Ser Asn Val Ala Thr Thr Lys Arg Pro Ala Gly Ser Ser Lys Val
1 5 10 15

Arg Val Val Pro Ser Arg Tyr Ser Ile Pro Pro Gly Ser Ser Leu Ala
20 25 30

Ala Val Thr Gln Gly Asn Arg Cys Lys Gln Ser Leu Pro Gly Ser Ala
35 40 45

Thr Glu Thr Arg Val Asn Leu Thr Glu Pro Pro Asn Asp Glu Leu Ser
50 55 60

Pro Glu Glu Leu Ala Lys Val Ala Glu Leu Leu Pro Arg Ile Arg Thr
65 70 75 80

Met Pro Pro Ser Asp Glu Ser Pro Arg Asp Ser Gly Cys Ala Lys Arg
85 90 95

Val Ala Asp Leu Val Gly Lys Arg Ser Phe Phe Thr Ala Ala Gly Asp
100 105 110

Asp Gly Asn Leu Val Thr Pro Tyr Gln Ala Arg Val Val Glu Leu Glu
115 120 125

Ser Pro Glu Ala Ala Ala Glu Glu Ala Glu Ala
130 135

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<211> 133
<212> PRT
<213> Saccharum sp.

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Thr Ser Asn Ala Ala Thr Ala Lys Arg Pro Ala Gly Ser Ser Lys Val
1 5 10 15

Arg Val Val Pro Ser Arg Tyr Ser Ile Thr Pro Gly Ser Tyr Leu Ala
20 25 30

Ala Val Ser Gln Asp Lys Arg Ser Lys Gln Ser Leu Pro Gly Pro Ala
35 40 45

Ser Ala Ala Ser Gln Arg Glu Glu Ile Arg Ala Lys Leu Thr Glu Pro
50 55 60

Ser Lys Asp Glu Leu Ser Pro Glu Thr Val Ala Lys Val Ala Glu Leu
65 70 75 80

Leu Pro Arg Ile Lys Thr Met Pro Ala Ser Asp Glu Ser Pro Arg Asp
85 90 95

Ser Ser Cys Ala Lys Arg Val Ala Asp Leu Val Gly Lys Arg Ser Phe
100 105 110

Phe Thr Xaa Ala Ala Glu Asp Gly Asn Phe Val Thr Pro Tyr Gln Ala
115 120 125

Pro Val Gly Glu Leu
130

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Xaa Glu Ala Arg Ile Val Phe Gly Thr Gly Asn Ser Ala Ile Met Ala
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Gly Gly Thr Lys Ala Pro Asp Thr Leu Glu Arg His Lys Met Lys Leu
20 25 30

Pro Lys Ile Lys Thr Val Arg Phe Thr Thr Glu Ser Pro Arg Asp Ser
35 40 45

Gly Cys Ile Lys Arg Glu Ile Asp Arg Ile Gly Lys Lys Ser Phe Phe
50 55 60

Ala Pro Asp Gly Ile Thr Ser Thr Pro Ser Ile Asp Xaa Xaa Asp Ala
65 70 75 80

Gly Lys Pro Leu Arg Arg Glu Ser Val His Glu Ile Xaa His Ala Xaa
85 90 95

Xaa Xaa

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Motif 1 CORE peptide

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Trp Xaa Asn Ala Xaa Xaa Asp
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Motif 3 (coiled core) CORE peptide

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<223> Any amino acid and this region may encompass 1 to 6 residues

<220>

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<222> (9)..(10)

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<222> (17)..(18)

<223> Any amino acid

<400> 36

Glu	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Glu	Xaa	Xaa	Arg	Leu	Xaa	Xaa	Xaa	Leu
1				5					10					15	

Xaa	Xaa	Leu	Arg
			20

<210> 37

<211> 29

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic Motif 4 CORE peptide

<220>

<221> MOD_RES

<222> (3)..(3)

<223> Any amino acid

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<222> (5)..(14)

<223> Any amino acid and this region may encompass 1 to 10 residues

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<222> (19)..(20)

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<222> (23)..(28)

<223> Any amino acid and this region may encompass 1 to 6 residues

<400> 37

Leu	Pro	Xaa	Ile	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Arg	Asp
1				5					10							15

Ser	Gly	Xaa	Xaa	Lys	Arg	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Lys
			20					25				